



1600

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RAW SEQUENCE LISTING

DATE: 03/27/2003

PATENT APPLICATION: US/09/634,109D

TIME: 12:39:13

Input Set : A:\6202NCP.txt

Output Set: N:\CRF4\03272003\I634109D.raw

4 <110> APPLICANT: Gabriel Vogeli
 5 Linda S. Wood
 7 <120> TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR EXPRESSED IN BRAIN
 9 <130> FILE REFERENCE: 28341/6202NCP
 11 <140> CURRENT APPLICATION NUMBER: US 09/634,109D
 12 <141> CURRENT FILING DATE: 2000-08-08
 14 <150> PRIOR APPLICATION NUMBER: US 09/377,563
 15 <151> PRIOR FILING DATE: 2000-08-19
 17 <160> NUMBER OF SEQ ID NOS: 14
 19 <170> SOFTWARE: PatentIn Ver. 2.0
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 948
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Homo sapiens
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (1)..(945)
 30 <400> SEQUENCE: 1
 31 atg gga aga tgg gtg aac cag tcc tac aca gat ggc ttc ttc ctc ttg 48
 32 Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
 33 1 5 10 15
 35 ggc atc ttt tcc cac agc cag act gac ctt gtc ctc ttc tct gca gtt 96
 36 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
 37 20 25 30
 39 atg gtg gtc ttc aca gtg gcc ctc tgt ggg aat gtc ctc ctc atc ttc 144
 40 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Ile Phe
 41 35 40 45
 43 ctc atc tac ctg gac gct gga ctt cac acc ccc atg tac ttc ttc ctc 192
 44 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
 45 50 55 60
 47 agc cag ctc tcc ctc atg gac ctc atg ttg gtc tgt aac att gtg cca 240
 48 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
 49 65 70 75 80
 51 aag atg gca gcc aac ttc ctg tct ggc agg aag tcc atc tcc ttt gtg 288
 52 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
 53 85 90 95
 55 ggc tgt ggc ata caa att ggc ttt ttt gtc tct ctt gtg gga tct gag 336
 56 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
 57 100 105 110
 59 ggg ctc ttg ctg gga ctc atg gct tat gac cac tac gtg gcc gtt agc 384
 60 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser
 61 115 120 125
 64 cac cca ctt cac tat ccc atc ctc atg aat cag agg gtc tgt ctc cag 432

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65 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
66      130                      135                      140
68 att act ggg agc tcc tgg gcc ttt ggg ata ata gat gga gtg att cag      480
69 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
70 145                      150                      155                      160
72 atg gtg gca gcc atg ggc tta cct tac tgt ggc tca agg agc gtg gat      528
73 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
74                      165                      170                      175
76 cac ttt ttc tgt gag gta caa gct tta ttg aag ctg gcc tgt gca gac      576
77 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
78      180                      185                      190
80 act tcc ctt ttt gac acc ctc ctc ttt gct tgc tgt gtc ttc atg ctt      624
81 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
82      195                      200                      205
84 ctc ctt ccc ttc tcc atc atc atg gcc tcc tat gct tgc atc cta ggg      672
85 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
86      210                      215                      220
88 gct gtg ctc cga ata cgc tct gct cag gcc tgg aaa aaa gcc ctg gcc      720
89 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
90 225                      230                      235                      240
92 acc tgc tcc tcc cac cta aca gct gtc acc ctc ttc tat ggg gca gcc      768
93 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
94      245                      250                      255
96 atg ttc atg tac ctg agg cct agg cgc tac cgg gcc cct agc cat gac      816
97 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
98      260                      265                      270
100 aag gtg gcc tct atc ttc tac aca gtc ctt act ccc atg ctg aac ccc      864
101 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
102      275                      280                      285
104 ctc att tac agc ttg agg aat ggg gag gtg atg ggg gca ctg agg aag      912
105 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
106      290                      295                      300
108 ggg ctg gac cgc tgc agg att ggc agc cag cac tga      948
109 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
110 305                      310                      315
113 <210> SEQ ID NO: 2
114 <211> LENGTH: 315
115 <212> TYPE: PRT
116 <213> ORGANISM: Homo sapiens
118 <400> SEQUENCE: 2
119 Met Gly Arg Trp Val Asn Gln Ser Tyr Thr Asp Gly Phe Phe Leu Leu
120 1 5 10 15
122 Gly Ile Phe Ser His Ser Gln Thr Asp Leu Val Leu Phe Ser Ala Val
123 20 25 30
126 Met Val Val Phe Thr Val Ala Leu Cys Gly Asn Val Leu Ile Phe
127 35 40 45
129 Leu Ile Tyr Leu Asp Ala Gly Leu His Thr Pro Met Tyr Phe Phe Leu
130 50 55 60
132 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro

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133 65 70 75 80
135 Lys Met Ala Ala Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Val
136 85 90 95
138 Gly Cys Gly Ile Gln Ile Gly Phe Phe Val Ser Leu Val Gly Ser Glu
139 100 105 110
141 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp His Tyr Val Ala Val Ser
142 115 120 125
144 His Pro Leu His Tyr Pro Ile Leu Met Asn Gln Arg Val Cys Leu Gln
145 130 135 140
147 Ile Thr Gly Ser Ser Trp Ala Phe Gly Ile Ile Asp Gly Val Ile Gln
148 145 150 155 160
150 Met Val Ala Ala Met Gly Leu Pro Tyr Cys Gly Ser Arg Ser Val Asp
151 165 170 175
153 His Phe Phe Cys Glu Val Gln Ala Leu Leu Lys Leu Ala Cys Ala Asp
154 180 185 190
156 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
157 195 200 205
159 Leu Leu Pro Phe Ser Ile Ile Met Ala Ser Tyr Ala Cys Ile Leu Gly
160 210 215 220
162 Ala Val Leu Arg Ile Arg Ser Ala Gln Ala Trp Lys Lys Ala Leu Ala
163 225 230 235 240
165 Thr Cys Ser Ser His Leu Thr Ala Val Thr Leu Phe Tyr Gly Ala Ala
166 245 250 255
168 Met Phe Met Tyr Leu Arg Pro Arg Arg Tyr Arg Ala Pro Ser His Asp
169 260 265 270
171 Lys Val Ala Ser Ile Phe Tyr Thr Val Leu Thr Pro Met Leu Asn Pro
172 275 280 285
174 Leu Ile Tyr Ser Leu Arg Asn Gly Glu Val Met Gly Ala Leu Arg Lys
175 290 295 300
177 Gly Leu Asp Arg Cys Arg Ile Gly Ser Gln His
178 305 310 315
181 <210> SEQ ID NO: 3
182 <211> LENGTH: 22
183 <212> TYPE: DNA
184 <213> ORGANISM: Artificial Sequence
186 <220> FEATURE:
187 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
188 SEQUENCE
190 <400> SEQUENCE: 3
191 gcctctatct tctacacagt cc 22
194 <210> SEQ ID NO: 4
195 <211> LENGTH: 20
196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
201 SEQUENCE
203 <400> SEQUENCE: 4
204 ccaaaacctt taaaccatcc 20

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207 <210> SEQ ID NO: 5
208 <211> LENGTH: 59
209 <212> TYPE: DNA
210 <213> ORGANISM: Artificial Sequence
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
214     SEQUENCE
216 <400> SEQUENCE: 5
217 gcactagtaa tacgactcac tatagggaga ccaccatggg aagatgggtg aaccagtcc 59
220 <210> SEQ ID NO: 6
221 <211> LENGTH: 60
222 <212> TYPE: DNA
223 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
226 <223> OTHER INFORMATION: Description of Artificial Sequence: PRIMER
227     SEQUENCE
229 <400> SEQUENCE: 6
230 gactggatcc cccgggcttt tttttttttt ttgcggccgc tcagtgctgg ctgccaatcc 60
233 <210> SEQ ID NO: 7
234 <211> LENGTH: 9
235 <212> TYPE: PRT
236 <213> ORGANISM: Artificial Sequence
238 <220> FEATURE:
239 <223> OTHER INFORMATION: Description of Artificial Sequence: MAP KINASE
240     SUBSTRATE PEPTIDE
242 <400> SEQUENCE: 7
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244   1           5
247 <210> SEQ ID NO: 8
248 <211> LENGTH: 316
249 <212> TYPE: PRT
250 <213> ORGANISM: Homo sapiens
252 <400> SEQUENCE: 8
253 Met Asp Asn Gln Ser Ser Thr Pro Gly Phe Leu Leu Leu Gly Phe Ser
254   1           5           10           15
256 Glu His Pro Gly Leu Gly Arg Thr Leu Phe Val Asp Val Ile Thr Ser
257           20           25           30
259 Tyr Leu Leu Thr Leu Val Gly Asn Thr Leu Ile Ile Leu Leu Ser Ala
260           35           40           45
262 Leu Asp Thr Lys Leu His Ser Pro Met Tyr Phe Phe Leu Ser Asn Leu
263           50           55           60
265 Ser Phe Leu Asp Leu Cys Phe Thr Thr Ser Cys Val Pro Gln Met Leu
266   65           70           75           80
268 Ala Asn Leu Trp Gly Pro Lys Lys Thr Ile Ser Phe Leu Asp Cys Ser
269           85           90           95
271 Val Gln Ile Phe Ile Phe Leu Ser Leu Gly Thr Thr Glu Cys Ile Leu
272           100          105          110
274 Met Lys Val Met Ala Phe Asp Arg Tyr Val Ala Val Cys Gln Pro Leu
275           115          120          125

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277 His Tyr Ala Thr Ile Ile His Pro Arg Leu Cys Trp Gln Leu Ala Ser
278      130                      135                      140
281 Val Ala Trp Val Ile Gly Leu Val Gly Ser Val Val Gln Thr Pro Ser
282 145                      150                      155                      160
284 Thr Leu His Leu Pro Phe Cys Pro Asp Arg Gln Val Asp Asp Phe Val
285                      165                      170                      175
287 Cys Glu Val Pro Ala Leu Ile Arg Leu Ser Cys Glu Asp Thr Ser Tyr
288                      180                      185                      190
290 Asn Glu Ile Gln Val Ala Val Ala Ser Val Phe Ile Leu Val Val Pro
291      195                      200                      205
293 Leu Ser Leu Ile Leu Val Ser Tyr Gly Ala Ile Thr Trp Ala Val Leu
294      210                      215                      220
296 Arg Ile Asn Ser Ala Thr Ala Trp Arg Lys Ala Phe Gly Thr Cys Ser
297 225                      230                      235                      240
299 Ser His Leu Thr Val Val Thr Leu Phe Tyr Ser Ser Val Ile Ala Val
300      245                      250                      255
302 Tyr Leu Gln Pro Lys Asn Pro Tyr Ala Gln Gly Arg Gly Lys Phe Phe
303      260                      265                      270
305 Gly Leu Phe Tyr Ala Val Gly Thr Pro Ser Leu Asn Pro Leu Val Tyr
306      275                      280                      285
308 Thr Leu Arg Asn Lys Glu Ile Lys Arg Ala Leu Arg Arg Leu Leu Gly
309      290                      295                      300
312 Lys Glu Arg Asp Ser Arg Glu Ser Trp Arg Ala Ala
313 305                      310                      315
316 <210> SEQ ID NO: 9
317 <211> LENGTH: 223
318 <212> TYPE: PRT
319 <213> ORGANISM: Mus musculus
321 <400> SEQUENCE: 9
322 Ser Gln Leu Ser Leu Met Asp Leu Met Leu Val Cys Asn Ile Val Pro
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325 Lys Met Ala Val Asn Phe Leu Ser Gly Arg Lys Ser Ile Ser Phe Ala
326      20      25      30
328 Gly Cys Gly Ile Gln Ile Gly Phe Val Ser Leu Val Gly Ser Glu
329      35      40      45
331 Gly Leu Leu Leu Gly Leu Met Ala Tyr Asp Arg Tyr Val Ala Ile Ser
332      50      55      60
334 His Pro Leu His Tyr Pro Ile Leu Met Ser Gln Lys Val Cys Leu Gln
335      65      70      75      80
337 Ile Ala Gly Ser Ser Trp Ala Phe Gly Ile Leu Asp Gly Ile Ile Gln
338      85      90      95
340 Met Val Ala Ala Met Ser Leu Pro Tyr Cys Gly Ser Arg Tyr Ile Asp
341      100     105     110
343 His Phe Phe Cys Glu Val Pro Ala Leu Leu Lys Leu Ala Cys Ala Asp
344      115     120     125
346 Thr Ser Leu Phe Asp Thr Leu Leu Phe Ala Cys Cys Val Phe Met Leu
347      130     135     140
349 Leu Leu Pro Phe Ser Ile Ile Val Thr Ser Tyr Ala Arg Ile Leu Gly
350 145     150     155     160

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VERIFICATION SUMMARY

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Input Set : A:\6202NCP.txt

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